



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Lau, Lester F.
- (ii) TITLE OF INVENTION: Extracellular Matrix Signalling Molecules
- (iii) NUMBER OF SEQUENCES: 21
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Howrey Simon Arnold & White LLP
 - (B) STREET: 321 North Clark Street, Suite 3400
 - (C) CITY: Chicago
 - (D) STATE: Illinois
 - (E) COUNTRY: United States of America
 - (F) ZIP: 60610
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 10/053,753
 - (B) FILING DATE: January 22, 2002
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Clough, David W.
 - (B) REGISTRATION NUMBER: 36,107
 - (C) REFERENCE/DOCKET NUMBER: 05031.0003.CNUS02
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 312/595-1408
 - (B) TELEFAX: 312/595-2250
 - (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1480 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 180..1316
- (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (D) OTHER INFORMATION: "Mouse cyr61 cDNA coding sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGAGAGCGCC CCAGAGAAGC GCCTGCAATC TCTGCGCCTC CTCCGCCAGC ACCTCGAGAG	60
AAGGACACCC GCCGCCTCGG CCCTCGCCTC ACCGCACTCC GGGCGCATTT GATCCCGCTG	120
CTCGCCGGCT TGTTGGTTCT GTGTCGCCGC GCTCGCCCCG GTTCCTCCTG CGCGCCACA	179
ATG AGC TCC AGC ACC TTC AGG ACG CTC GCT GTC GCC GTC ACC CTT CTC Met Ser Ser Ser Thr Phe Arg Thr Leu Ala Val Ala Val Thr Leu Leu 1 5 10 15	227
CAC TTG ACC AGA CTG GCG CTC TCC ACC TGC CCC GCC GCC TGC CAC TGC His Leu Thr Arg Leu Ala Leu Ser Thr Cys Pro Ala Ala Cys His Cys 20 25 30	275
CCT CTG GAG GCA CCC AAG TGC GCC CCG GGA GTC GGG TTG GTC CGG GAC Pro Leu Glu Ala Pro Lys Cys Ala Pro Gly Val Gly Leu Val Arg Asp 35 40 45	323
GGC TGC GGC TGC TGT AAG GTC TGC GCT AAA CAA CTC AAC GAG GAC TGC Gly Cys Gly Cys Cys Lys Val Cys Ala Lys Gln Leu Asn Glu Asp Cys 50 55 60	371
AGC AAA ACT CAG CCC TGC GAC CAC ACC AAG GGG TTG GAA TGC AAT TTC Ser Lys Thr Gln Pro Cys Asp His Thr Lys Gly Leu Glu Cys Asn Phe 65 70 75 80	419
GGC GCC AGC TCC ACC GCT CTG AAA GGG ATC TGC AGA GCT CAG TCA GAA Gly Ala Ser Ser Thr Ala Leu Lys Gly Ile Cys Arg Ala Gln Ser Glu 85 90 95	467
GGC AGA CCC TGT GAA TAT AAC TCC AGA ATC TAC CAA AAC GGG GAA AGC Gly Arg Pro Cys Glu Tyr Asn Ser Arg Ile Tyr Gln Asn Gly Glu Ser 100 105 110	515
TTC CAG CCC AAC TGT AAA CAC CAG TGC ACA TGT ATT GAT GGC GCC GTG Phe Gln Pro Asn Cys Lys His Gln Cys Thr Cys Ile Asp Gly Ala Val 115 120 125	563
GGC TGC ATT CCT CTG TGT CCC CAA GAA CTG TCT CTC CCC AAT CTG GGC Gly Cys Ile Pro Leu Cys Pro Gln Glu Leu Ser Leu Pro Asn Leu Gly 130 135 140	611
TGT CCC AAC CCC CGG CTG GTG AAA GTC AGC GGG CAG TGC TGT GAA GAG Cys Pro Asn Pro Arg Leu Val Lys Val Ser Gly Gln Cys Cys Glu Glu 145 150 155 160	659
TGG GTT TGT GAT GAA GAC AGC ATT AAG GAC TCC CTG GAC GAC CAG GAT Trp Val Cys Asp Glu Asp Ser Ile Lys Asp Ser Leu Asp Asp Gln Asp 165 170 175	707
GAC CTC CTC GGA CTC GAT GCC TCG GAG GTG GAG TTA ACG AGA AAC AAT Asp Leu Leu Gly Leu Asp Ala Ser Glu Val Glu Leu Thr Arg Asn Asn 180 185 190	755

GAG TTA ATC GCA ATT GGA AAA GGC AGC TCA CTG AAG AGG CTT CCT GTC Glu Leu Ile Ala Ile Gly Lys Gly Ser Ser Leu Lys Arg Leu Pro Val 195 200 205	803
TTT GGC ACC GAA CCG CGA GTT CTT TTC AAC CCT CTG CAC GCC CAT GGC Phe Gly Thr Glu Pro Arg Val Leu Phe Asn Pro Leu His Ala His Gly 210 215 220	851
CAG AAA TGC ATC GTT CAG ACC ACG TCT TGG TCC CAG TGC TCC AAG AGC Gln Lys Cys Ile Val Gln Thr Thr Ser Trp Ser Gln Cys Ser Lys Ser 225 230 235 240	899
TGC GGA ACT GGC ATC TCC ACA CGA GTT ACC AAT GAC AAC CCA GAG TGC Cys Gly Thr Gly Ile Ser Thr Arg Val Thr Asn Asp Asn Pro Glu Cys 245 250 255	947
CGC CTG GTG AAA GAG ACC CGG ATC TGT GAA GTG CGT CCT TGT GGA CAA Arg Leu Val Lys Glu Thr Arg Ile Cys Glu Val Arg Pro Cys Gly Gln 260 265 270	995
CCA GTG TAC AGC AGC CTA AAA AAG GGC AAG AAA TGC AGC AAG ACC AAG Pro Val Tyr Ser Ser Leu Lys Lys Gly Lys Lys Cys Ser Lys Thr Lys 275 280 285	1043
AAA TCC CCA GAA CCA GTC AGA TTT ACT TAT GCA GGA TGC TCC AGT GTC Lys Ser Pro Glu Pro Val Arg Phe Thr Tyr Ala Gly Cys Ser Ser Val 290 295 300	1091
AAG AAA TAC CGG CCC AAA TAC TGC GGC TCC TGC GTA GAT GGC CGG TGC Lys Lys Tyr Arg Pro Lys Tyr Cys Gly Ser Cys Val Asp Gly Arg Cys 305 310 315 320	1139
TGC ACA CCT CTG CAG ACC AGA ACT GTG AAG ATG CGG TTC CGA TGC GAA Cys Thr Pro Leu Gln Thr Arg Thr Val Lys Met Arg Phe Arg Cys Glu 325 330 335	1187
GAT GGA GAG ATG TTT TCC AAG AAT GTC ATG ATG ATC CAG TCC TGC AAA Asp Gly Glu Met Phe Ser Lys Asn Val Met Met Ile Gln Ser Cys Lys 340 345 350	1235
TGT AAC TAC AAC TGC CCG CAT CCC AAC GAG GCA TCG TTC CGA CTG TAC Cys Asn Tyr Asn Cys Pro His Pro Asn Glu Ala Ser Phe Arg Leu Tyr 355 360 365	1283
AGC CTA TTC AAT GAC ATC CAC AAG TTC AGG GAC TAAGTGCCTC CAGGGTTCCT Ser Leu Phe Asn Asp Ile His Lys Phe Arg Asp 370 375	1336
AGTGTGGGCT GGACAGAGGA GAAGCGCAAG CATCATGGAG ACGTGGGTGG GCGGAGGATG	1396
AATGGTGCCT TGCTCATTCT TGAGTAGCAT TAGGGTATTT CAAAAGTACC AAGGGGCTGA	1456
TGTGGACGGA CAGCAGCGCA GCCG	1480

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 379 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(D) OTHER INFORMATION: "Mouse Cyr61 amino acid sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Ser	Ser	Ser	Thr	Phe	Arg	Thr	Leu	Ala	Val	Ala	Val	Thr	Leu	Leu	
1				5				10						15		
His	Leu	Thr	Arg	Leu	Ala	Leu	Ser	Thr	Cys	Pro	Ala	Ala	Cys	His	Cys	
			20					25					30			
Pro	Leu	Glu	Ala	Pro	Lys	Cys	Ala	Pro	Gly	Val	Gly	Leu	Val	Arg	Asp	
		35					40					45				
Gly	Cys	Gly	Cys	Cys	Lys	Val	Cys	Ala	Lys	Gln	Leu	Asn	Glu	Asp	Cys	
	50					55					60					
Ser	Lys	Thr	Gln	Pro	Cys	Asp	His	Thr	Lys	Gly	Leu	Glu	Cys	Asn	Phe	
65					70					75					80	
Gly	Ala	Ser	Ser	Thr	Ala	Leu	Lys	Gly	Ile	Cys	Arg	Ala	Gln	Ser	Glu	
				85					90					95		
Gly	Arg	Pro	Cys	Glu	Tyr	Asn	Ser	Arg	Ile	Tyr	Gln	Asn	Gly	Glu	Ser	
		100						105					110			
Phe	Gln	Pro	Asn	Cys	Lys	His	Gln	Cys	Thr	Cys	Ile	Asp	Gly	Ala	Val	
	115						120					125				
Gly	Cys	Ile	Pro	Leu	Cys	Pro	Gln	Glu	Leu	Ser	Leu	Pro	Asn	Leu	Gly	
	130					135					140					
Cys	Pro	Asn	Pro	Arg	Leu	Val	Lys	Val	Ser	Gly	Gln	Cys	Cys	Glu	Glu	
145					150					155				160		
Trp	Val	Cys	Asp	Glu	Asp	Ser	Ile	Lys	Asp	Ser	Leu	Asp	Asp	Gln	Asp	
			165						170					175		
Asp	Leu	Leu	Gly	Leu	Asp	Ala	Ser	Glu	Val	Glu	Leu	Thr	Arg	Asn	Asn	
			180					185					190			
Glu	Leu	Ile	Ala	Ile	Gly	Lys	Gly	Ser	Ser	Leu	Lys	Arg	Leu	Pro	Val	
	195						200					205				
Phe	Gly	Thr	Glu	Pro	Arg	Val	Leu	Phe	Asn	Pro	Leu	His	Ala	His	Gly	
	210					215					220					
Gln	Lys	Cys	Ile	Val	Gln	Thr	Thr	Ser	Trp	Ser	Gln	Cys	Ser	Lys	Ser	
225					230					235				240		

Cys Gly Thr Gly Ile Ser Thr Arg Val Thr Asn Asp Asn Pro Glu Cys
 245 250 255
 Arg Leu Val Lys Glu Thr Arg Ile Cys Glu Val Arg Pro Cys Gly Gln
 260 265 270
 Pro Val Tyr Ser Ser Leu Lys Lys Gly Lys Lys Cys Ser Lys Thr Lys
 275 280 285
 Lys Ser Pro Glu Pro Val Arg Phe Thr Tyr Ala Gly Cys Ser Ser Val
 290 295 300
 Lys Lys Tyr Arg Pro Lys Tyr Cys Gly Ser Cys Val Asp Gly Arg Cys
 305 310 315 320
 Cys Thr Pro Leu Gln Thr Arg Thr Val Lys Met Arg Phe Arg Cys Glu
 325 330 335
 Asp Gly Glu Met Phe Ser Lys Asn Val Met Met Ile Gln Ser Cys Lys
 340 345 350
 Cys Asn Tyr Asn Cys Pro His Pro Asn Glu Ala Ser Phe Arg Leu Tyr
 355 360 365
 Ser Leu Phe Asn Asp Ile His Lys Phe Arg Asp
 370 375

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1418 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 124..1266

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (D) OTHER INFORMATION: "Human cyr61 cDNA coding sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGGCGGGCCC ACCGCGACAC CGCGCCGCCA CCCCACCCCC GCTGCGCACG GCCTGTCCGC	60
TGCACACCAG CTTGTTGGCG TCTTCGTCGC CGCGCTCGCC CCGGGCTACT CCTGCGCGCC	120
ACA ATG AGC TCC CGC ATC GCC AGG GCG CTC GCC TTA GTC GTC ACC CTT	168
Met Ser Ser Arg Ile Ala Arg Ala Leu Ala Leu Val Val Thr Leu	
1 5 10 15	
CTC CAC TTG ACC AGG CTG GCG CTC TCC ACC TGC CCC GCT GCC TGC CAC	216
Leu His Leu Thr Arg Leu Ala Leu Ser Thr Cys Pro Ala Ala Cys His	

	20	25	30	
TGC CCC CTG GAG GCG CCC AAG TGC GCG CCG GGA GTC GGG CTG GTC CGG				264
Cys Pro Leu Glu Ala Pro Lys Cys Ala Pro Gly Val Gly Leu Val Arg				
	35	40	45	
GAC GGC TGC GGC TGC TGT AAG GTC TGC GCC AAG CAG CTC AAC GAG GAC				312
Asp Gly Cys Gly Cys Cys Lys Val Cys Ala Lys Gln Leu Asn Glu Asp				
	50	55	60	
TGC AGC AAA ACG CAG CCC TGC GAC CAC ACC AAG GGG CTG GAA TGC AAC				360
Cys Ser Lys Thr Gln Pro Cys Asp His Thr Lys Gly Leu Glu Cys Asn				
	65	70	75	
TTC GGC GCC AGC TCC ACC GCT CTG AAG GGG ATC TGC AGA GCT CAG TCA				408
Phe Gly Ala Ser Ser Thr Ala Leu Lys Gly Ile Cys Arg Ala Gln Ser				
	80	85	90	95
GAG GGC AGA CCC TGT GAA TAT AAC TCC AGA ATC TAC CAA AAC GGG GAA				456
Glu Gly Arg Pro Cys Glu Tyr Asn Ser Arg Ile Tyr Gln Asn Gly Glu				
	100	105	110	
AGT TTC CAG CCC AAC TGT CAA CAT CAG TGC ACA TGT ATT GAT GGC GCC				504
Ser Phe Gln Pro Asn Cys Gln His Gln Cys Thr Cys Ile Asp Gly Ala				
	115	120	125	
GTG GGC TGC ATT CCT CTG TGT CCC CAA GAA CTA TCT CTC CCC AAC TTG				552
Val Gly Cys Ile Pro Leu Cys Pro Gln Glu Leu Ser Leu Pro Asn Leu				
	130	135	140	
GGC TGT CCC AAC CCT CGG CTG GTC AAA GTT ACC GGG CAG TGC TGC GAG				600
Gly Cys Pro Asn Pro Arg Leu Val Lys Val Thr Gly Gln Cys Cys Glu				
	145	150	155	
GAG TGG GTC TGT GAC GAG GAT AGT ATC AAG GAC CCC ATG GAG GAC CAG				648
Glu Trp Val Cys Asp Glu Asp Ser Ile Lys Asp Pro Met Glu Asp Gln				
	160	165	170	175
GAC GGC CTC CTT GGC AAG GAG CTG GGA TTC GAT GCC TCC GAG GTG GAG				696
Asp Gly Leu Leu Gly Lys Glu Leu Gly Phe Asp Ala Ser Glu Val Glu				
	180	185	190	
TTG ACG AGA AAC AAT GAA TTG ATT GCA GTT GGA AAA GGC AGA TCA CTG				744
Leu Thr Arg Asn Asn Glu Leu Ile Ala Val Gly Lys Gly Arg Ser Leu				
	195	200	205	
AAG CGG CTC CCT GTT TTT GGA ATG GAG CCT CGC ATC CTA TAC AAC CCT				792
Lys Arg Leu Pro Val Phe Gly Met Glu Pro Arg Ile Leu Tyr Asn Pro				
	210	215	220	
TTA CAA GGC CAG AAA TGT ATT GTT CAA ACA ACT TCA TGG TCC CAG TGC				840
Leu Gln Gly Gln Lys Cys Ile Val Gln Thr Thr Ser Trp Ser Gln Cys				
	225	230	235	
TCA AAG ACC TGT GGA ACT GGT ATC TCC ACA CGA GTT ACC AAT GAC AAC				888
Ser Lys Thr Cys Gly Thr Gly Ile Ser Thr Arg Val Thr Asn Asp Asn				
	240	245	250	255

CCT GAG TGC CGC CTT GTG AAA GAA ACC CGG ATT TGT GAG GTG CGG CCT	936
Pro Glu Cys Arg Leu Val Lys Glu Thr Arg Ile Cys Glu Val Arg Pro	
260 265 270	
TGT GGA CAG CCA GTG TAC AGC AGC CTG AAA AAG GGC AAG AAA TGC AGC	984
Cys Gly Gln Pro Val Tyr Ser Ser Leu Lys Lys Gly Lys Lys Cys Ser	
275 280 285	
AAG ACC AAG AAA TCC CCC GAA CCA GTC AGG TTT ACT TAC GCT GGA TGT	1032
Lys Thr Lys Lys Ser Pro Glu Pro Val Arg Phe Thr Tyr Ala Gly Cys	
290 295 300	
TTG AGT GTG AAG AAA TAC CGG CCC AAG TAC TGC GGT TCC TGC GTG GAC	1080
Leu Ser Val Lys Lys Tyr Arg Pro Lys Tyr Cys Gly Ser Cys Val Asp	
305 310 315	
GGC CGA TGC TGC ACG CCC CAG CTG ACC AGG ACT GTG AAG ATG CGG TTC	1128
Gly Arg Cys Cys Thr Pro Gln Leu Thr Arg Thr Val Lys Met Arg Phe	
320 325 330 335	
CGC TGC GAA GAT GGG GAG ACA TTT TCC AAG AAC GTC ATG ATG ATC CAG	1176
Arg Cys Glu Asp Gly Glu Thr Phe Ser Lys Asn Val Met Met Ile Gln	
340 345 350	
TCC TGC AAA TGC AAC TAC AAC TGC CCG CAT GCC AAT GAA GCA GCG TTT	1224
Ser Cys Lys Cys Asn Tyr Asn Cys Pro His Ala Asn Glu Ala Ala Phe	
355 360 365	
CCC TTC TAC AGG CTG TTC AAT GAC ATT CAC AAA TTT AGG GAC	1266
Pro Phe Tyr Arg Leu Phe Asn Asp Ile His Lys Phe Arg Asp	
370 375 380	
TAAATGCTAC CTGGGTTTCC AGGGCACACC TAGACAAACA AGGGAGAAGA GTGTCAGAAT	1326
CAGAATCATG GAGAAAATGG GCGGGGGTGG TGTGGGTGAT GGGACTCATT GTAGAAAGGA	1386
AGCCTTCTCA TTCTTGAGGA GCATTAAGGT AT	1418

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (D) OTHER INFORMATION: "Human Cyr61 amino acid sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Ser	Ser	Arg	Ile	Ala	Arg	Ala	Leu	Ala	Leu	Val	Val	Thr	Leu	Leu
1					5				10					15	

His	Leu	Thr	Arg	Leu	Ala	Leu	Ser	Thr	Cys	Pro	Ala	Ala	Cys	His	Cys	
			20					25					30			
Pro	Leu	Glu	Ala	Pro	Lys	Cys	Ala	Pro	Gly	Val	Gly	Leu	Val	Arg	Asp	
		35					40					45				
Gly	Cys	Gly	Cys	Cys	Lys	Val	Cys	Ala	Lys	Gln	Leu	Asn	Glu	Asp	Cys	
	50					55					60					
Ser	Lys	Thr	Gln	Pro	Cys	Asp	His	Thr	Lys	Gly	Leu	Glu	Cys	Asn	Phe	
65					70					75					80	
Gly	Ala	Ser	Ser	Thr	Ala	Leu	Lys	Gly	Ile	Cys	Arg	Ala	Gln	Ser	Glu	
				85					90					95		
Gly	Arg	Pro	Cys	Glu	Tyr	Asn	Ser	Arg	Ile	Tyr	Gln	Asn	Gly	Glu	Ser	
		100						105					110			
Phe	Gln	Pro	Asn	Cys	Gln	His	Gln	Cys	Thr	Cys	Ile	Asp	Gly	Ala	Val	
		115					120					125				
Gly	Cys	Ile	Pro	Leu	Cys	Pro	Gln	Glu	Leu	Ser	Leu	Pro	Asn	Leu	Gly	
	130					135					140					
Cys	Pro	Asn	Pro	Arg	Leu	Val	Lys	Val	Thr	Gly	Gln	Cys	Cys	Glu	Glu	
145					150					155					160	
Trp	Val	Cys	Asp	Glu	Asp	Ser	Ile	Lys	Asp	Pro	Met	Glu	Asp	Gln	Asp	
			165						170					175		
Gly	Leu	Leu	Gly	Lys	Glu	Leu	Gly	Phe	Asp	Ala	Ser	Glu	Val	Glu	Leu	
		180						185					190			
Thr	Arg	Asn	Asn	Glu	Leu	Ile	Ala	Val	Gly	Lys	Gly	Arg	Ser	Leu	Lys	
		195					200					205				
Arg	Leu	Pro	Val	Phe	Gly	Met	Glu	Pro	Arg	Ile	Leu	Tyr	Asn	Pro	Leu	
	210					215					220					
Gln	Gly	Gln	Lys	Cys	Ile	Val	Gln	Thr	Thr	Ser	Trp	Ser	Gln	Cys	Ser	
225					230					235					240	
Lys	Thr	Cys	Gly	Thr	Gly	Ile	Ser	Thr	Arg	Val	Thr	Asn	Asp	Asn	Pro	
			245						250					255		
Glu	Cys	Arg	Leu	Val	Lys	Glu	Thr	Arg	Ile	Cys	Glu	Val	Arg	Pro	Cys	
		260						265					270			
Gly	Gln	Pro	Val	Tyr	Ser	Ser	Leu	Lys	Lys	Gly	Lys	Lys	Cys	Ser	Lys	
		275					280						285			
Thr	Lys	Lys	Ser	Pro	Glu	Pro	Val	Arg	Phe	Thr	Tyr	Ala	Gly	Cys	Leu	
	290					295					300					
Ser	Val	Lys	Lys	Tyr	Arg	Pro	Lys	Tyr	Cys	Gly	Ser	Cys	Val	Asp	Gly	
305					310					315					320	

Arg Cys Cys Thr Pro Gln Leu Thr Arg Thr Val Lys Met Arg Phe Arg
325 330 335

Cys Glu Asp Gly Glu Thr Phe Ser Lys Asn Val Met Met Ile Gln Ser
340 345 350

Cys Lys Cys Asn Tyr Asn Cys Pro His Ala Asn Glu Ala Ala Phe Pro
355 360 365

Phe Tyr Arg Leu Phe Asn Asp Ile His Lys Phe Arg Asp
370 375 380

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (D) OTHER INFORMATION: "Fisp12 cDNA coding sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAATTCCGCC GACAACCCCA GACGCCACCG CCTGGAGCGT CCAGACACCA ACCTCCGCCC	60
CTGTCCGAAT CCAGGCTCCA GCCGCGCCTC TCGTCGCCTC TGCACCCTGC TGTGCATCCT	120
CCTACCGCGT CCCGATCATG CTCGCCTCCG TCGCAGGTCC CATCAGCCTC GCCTTGGTGC	180
TCCTCGCCCT CTGCACCCGG CCTGCTACGG GCCAGGACTG CAGCGCGCAA TGTCAGTGCG	240
CAGCCGAAGC AGCGCCGCAC TGCCCCGCCG GCGTGAGCCT GGTGCTGGAC GGCTGCGGCT	300
GCTGCCGCGT CTGCGCCAAG CAGCTGGGAG AACTGTGTAC GGAGCGTGAC CCCTGCGACC	360
CACACAAGGG CCTCTTCTGC GATTTCGGCT CCCCCGCCAA CCGCAAGATT GGAGTGTGCA	420
CTGCCAAAGA TGGTGACCC TGTGTCTTCG GTGGGTCGGT GTACCGCAGC GGTGAGTCCT	480
TCCAAAGCAG CTGCAAATAC CAATGCACTT GCCTGGATGG GGCCGTGGGC TGCGTGCCCC	540
TATGCAGCAT GGACGTGCGC CTGCCCAGCC CTGACTGCCC CTTCCCGAGA AGGGTCAAGC	600
TGCCTGGGAA ATGCTGCAAG GAGTGGGTGT GTGACGAGCC CAAGGACCGC ACAGCAGTTG	660
GCCCTGCCCT AGCTGCCTAC CGACTGGAAG ACACATTTGG CCCAGACCCA ACTATGATGC	720
GAGCCAACTG CCTGGTCCAG ACCACAGAGT GGAGCGCCTG TTCTAAGACC TGTGGAATGG	780
GCATCTCCAC CCGAGTTACC AATGACAATA CCTTCTGCAG ACTGGAGAAG CAGAGCCGCC	840
TCTGCATGGT CAGGCCCTGC GAAGCTGACC TGGAGGAAAA CATTAAGAAG GGCAAAAAGT	900

GCATCCGGAC	ACCTAAAATC	GCCAAGCCTG	TCAAGTTTGA	GCTTTCTGGC	TGCACCAGTG	960
TGAAGACATA	CAGGGCTAAG	TTCTGCGGGG	TGTGCACAGA	CGGCCGCTGC	TGCACACCGC	1020
ACAGAACCAC	CACTCTGCCA	GTGGAGTTCA	AATGCCCCGA	TGGCGAGATC	ATGAAAAAGA	1080
ATATGATGTT	CATCAAGACC	TGTGCCTGCC	ATTACAACTG	TCCTGGGGAC	AATGACATCT	1140
TTGAGTCCCT	GTACTACAGG	AAGATGTACG	GAGACATGGC	GTAAAGCCAG	GAAGTAAGGG	1200
ACACGAACTC	ATTAGACTAT	AACTTGAAct	GAGTTGCATC	TCATTTTCTT	CTGTAAAAAC	1260
AATTACAGTA	GCACATTAAT	TTAAATCTGT	GTTTTTAACT	ACCGTGGGAG	GAAGTATCCC	1320
ACCAAAGTGA	GAACGTTATG	TCATGGCCAT	ACAAGTAGTC	TGTCAACCTC	AGACACTGGT	1380
TTCGAGACAG	TTTACACTTG	ACAGTTGTTC	ATTAGCGCAC	AGTGCCAGAA	CGCACACTGA	1440
GGTGAGTCTC	CTGGAACAGT	GGAGATGCCA	GGAGAAAGAA	AGACAGGTAC	TAGCTGAGGT	1500
TATTTTAAAA	GCAGCAGTGT	GCCTACTTTT	TGGAGTGTA	CCGGGGAGGG	AAATTATAGC	1560
ATGCTTGCA	ACAGACCTGC	TCTAGCGAGA	GCTGAGCATG	TGTCCTCCAC	TAGATGAGGC	1620
TGAGTCCAGC	TGTTCTTTAA	GAACAGCAGT	TTCAGCCTCT	GACCATTCTG	ATTCCAGTGA	1680
CACTTGTCAG	GAGTCAGAGC	CTTGTCTGTT	AGACTGGACA	GCTTGTGGCA	AGTAAGTTTG	1740
CCTGTAACAA	GCCAGATTTT	TATTGATATT	GTAAATATTG	TGGATATATA	TATATATATA	1800
TATATTTGTA	CAGTTATCTA	AGTTAATTTA	AAGTCATTTG	TTTTTGTTTT	AAGTGCTTTT	1860
GGGATTTTAA	ACTGATAGCC	TCAAACCTCA	AACACCATAG	GTAGGACACG	AAGCTTATCT	1920
GTGATTCAAA	ACAAAGGAGA	TACTGCAGTG	GGAATTGTGA	CCTGAGTGAC	TCTCTGTCAG	1980
AACAAACAAA	TGCTGTGCAG	GTGATAAAGC	TATGTATTGG	AAGTCAGATT	TCTAGTAGGA	2040
AATGTGGTCA	AATCCCTGTT	GGTGAACAAA	TGGCCTTTAT	TAAGAAATGG	CTGGCTCAGG	2100
GTAAGGTCCG	ATTCCTACCA	GGAAGTGCTT	GCTGCTTCTT	TGATTATGAC	TGGTTTGGGG	2160
TGGGGGGCAG	TTTATTTGTT	GAGAGTGTGA	CCAAAAGTTA	CATGTTTGCA	CCTTTCTAGT	2220
TGAAAATAAA	GTATATATAT	ATTTTTTTATA	TGAAAAAAA	GGAATTC		2267

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(D) OTHER INFORMATION: "Fisp12 amino acid sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```
Met Leu Ala Ser Val Ala Gly Pro Ile Ser Leu Ala Leu Val Leu Leu
1           5           10           15

Ala Leu Cys Thr Arg Pro Ala Thr Gly Gln Asp Cys Ser Ala Gln Cys
20           25           30

Gln Cys Ala Ala Glu Ala Ala Pro His Cys Pro Ala Gly Val Ser Leu
35           40           45

Val Leu Asp Gly Cys Gly Cys Cys Arg Val Cys Ala Lys Gln Leu Gly
50           55           60

Glu Leu Cys Thr Glu Arg Asp Pro Cys Asp Pro His Lys Gly Leu Phe
65           70           75           80

Cys Asp Phe Gly Ser Pro Ala Asn Arg Lys Ile Gly Val Cys Thr Ala
85           90           95

Lys Asp Gly Ala Pro Cys Val Phe Gly Gly Ser Val Tyr Arg Ser Gly
100          105          110

Glu Ser Phe Gln Ser Ser Cys Lys Tyr Gln Cys Thr Cys Leu Asp Gly
115          120          125

Ala Val Gly Cys Val Pro Leu Cys Ser Met Asp Val Arg Leu Pro Ser
130          135          140

Pro Asp Cys Pro Phe Pro Arg Arg Val Lys Leu Pro Gly Lys Cys Cys
145          150          155          160

Lys Glu Trp Val Cys Asp Glu Pro Lys Asp Arg Thr Ala Val Gly Pro
165          170          175

Ala Leu Ala Ala Tyr Arg Leu Glu Asp Thr Phe Gly Pro Asp Pro Thr
180          185          190

Met Met Arg Ala Asn Cys Leu Val Gln Thr Thr Glu Trp Ser Ala Cys
195          200          205

Ser Lys Thr Cys Gly Met Gly Ile Ser Thr Arg Val Thr Asn Asp Asn
210          215          220

Thr Phe Cys Arg Leu Glu Lys Gln Ser Arg Leu Cys Met Val Arg Pro
225          230          235          240

Cys Glu Ala Asp Leu Glu Glu Asn Ile Lys Lys Gly Lys Lys Cys Ile
245          250          255

Arg Thr Pro Lys Ile Ala Lys Pro Val Lys Phe Glu Leu Ser Gly Cys
260          265          270
```

Thr	Ser	Val	Lys	Thr	Tyr	Arg	Ala	Lys	Phe	Cys	Gly	Val	Cys	Thr	Asp
		275					280					285			
Gly	Arg	Cys	Cys	Thr	Pro	His	Arg	Thr	Thr	Thr	Leu	Pro	Val	Glu	Phe
	290					295					300				
Lys	Cys	Pro	Asp	Gly	Glu	Ile	Met	Lys	Lys	Asn	Met	Met	Phe	Ile	Lys
	305				310					315					320
Thr	Cys	Ala	Cys	His	Tyr	Asn	Cys	Pro	Gly	Asp	Asn	Asp	Ile	Phe	Glu
				325					330					335	
Ser	Leu	Tyr	Tyr	Arg	Lys	Met	Tyr	Gly	Asp	Met	Ala				
					340			345							

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2075 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (D) OTHER INFORMATION: "CTGF cDNA coding sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CCCGGCCGAC AGCCCCGAGA CGACAGCCCG GCGCGTCCCG GTCCCCACCT CCGACCACCG	60
CCAGCGCTCC AGGCCCCGCG CTCCCCGCTC GCCGCCACCG CGCCCTCCGC TCCGCCCCGA	120
GTGCCAACCA TGACCGCCGC CAGTATGGGC CCCGTCCGCG TCGCCTTCGT GGTCTCCTC	180
GCCCTCTGCA GCCGGCCGGC CGTCGGCCAG AACTGCAGCG GGCCGTGCCG GTGCCCCGAC	240
GAGCCGGCGC CGCGCTGCCC GGCGGGCGTG AGCCTCGTGC TGGACGGCTG CGGCTGCTGC	300
CGCGTCTGCG CCAAGCAGCT GGGCGAGCTG TGCACCGAGC GCGACCCCTG CGACCCGCAC	360
AAGGGCCTCT TCTGTGACTT CGGCTCCCCG GCCAACCGCA AGATCGGCGT GTGCACCGCC	420
AAAGATGGTG CTCCCTGCAT CTTCCGTGGT ACGGTGTACC GCAGCGGAGA GTCCTTCCAG	480
AGCAGCTGCA AGTACCAGTG CACGTGCCTG GACGGGGCGG TGGGCTGCAT GCCCTGTGC	540
AGCATGGACG TTCGTCTGCC CAGCCCTGAC TGCCCCTTCC CGAGGAGGGT CAAGCTGCCC	600
GGGAAATGCT GCGAGGAGTG GGTGTGTGAC GAGCCCAAGG ACCAAACCGT GGTGGGGCCT	660
GCCCTCGCGG CTTACCGACT GGAAGACACG TTTGGCCCAG ACCCAACTAT GATTAGAGCC	720
AACTGCCTGG TCCAGACCAC AGAGTGGAGC GCCTGTTCCA AGACCTGTGG GATGGGCATC	780

TCCACCCGGG TTACCAATGA CAACGCCTCC TGCAGGCTAG AGAAGCAGAG CCGCCTGTGC	840
ATGGTCAGGC CTTGCGAAGC TGACCTGGAA GAGAACATTA AGAAGGGCAA AAAGTGCATC	900
CGTACTCCCA AAATCTCCAA GCCTATCAAG TTTGAGCTTT CTGGCTGCAC CAGCATGAAG	960
ACATACCGAG CTAAATTCTG TGGAGTATGT ACCGACGGCC GATGCTGCAC CCCCCACAGA	1020
ACCACCACCC TGCCGGTGGA GTTCAAGTGC CCTGACGGCG AGGTCATGAA GAAGAACATG	1080
ATGTTTCATCA AGACCTGTGC CTGCCATTAC AACTGTCCCG GAGACAATGA CATCTTTGAA	1140
TCGCTGTACT ACAGGAAGAT GTACGGAGAC ATGGCATGAA GCCAGAGAGT GAGAGACATT	1200
AACTCATTAG ACTGGAACTT GAACTGATTC ACATCTCATT TTTCCGTAAA AATGATTTCA	1260
GTAGCACAAG TTATTTAAAT CTGTTTTTCT AACTGGGGGA AAAGATTCCC ACCCAATTCA	1320
AAACATTGTG CCATGTCAAA CAAATAGTCT ATCTTCCCCA GACACTGGTT TGAAGAATGT	1380
TAAGACTTGA CAGTGGAAC ACATTAGTAC ACAGCACCAG AATGTATATT AAGGTGTGGC	1440
TTTAGGAGCA GTGGGAGGGT ACCGGCCCCG TTAGTATCAT CAGATCGACT CTTATACGAG	1500
TAATATGCCT GCTATTTGAA GTGTAATTGA GAAGGAAAAT TTTAGCGTGC TCACTGACCT	1560
GCCTGTAGCC CCAGTGACAG CTAGGATGTG CATTCTCCAG CCATCAAGAG ACTGAGTCAA	1620
GTTGTTCCCTT AAGTCAGAAC AGCAGACTCA GCTCTGACAT TCTGATTCTGA ATGACACTGT	1680
TCAGGAATCG GAATCCTGTC GATTAGACTG GACAGCTTGT GGCAAGTGAA TTTGCCTGTA	1740
ACAAGCCAGA TTTTTTAAAA TTTATATTGT AAATATTGTG TGTGTGTGTG TGTGTGTATA	1800
TATATATATA TATGTACAGT TATCTAAGTT AATTTAAAGT TGTTTGTGCC TTTTATTTT	1860
TGTTTTTAAT GCTTTGATAT TTCAATGTTA GCCTCAATTT CTGAACACCA TAGGTAGAAT	1920
GTAAAGCTTG TCTGATCGTT CAAAGCATGA AATGGATACT TATATGGAAA TTCTGCTCAG	1980
ATAGAATGAC AGTCCGTCAA AACAGATTGT TTGCAAAGGG GAGGCATCAG TGTCTTGGCA	2040
GGCTGATTTT TAGGTAGGAA ATGTGGTAGC TCACG	2075

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 349 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (D) OTHER INFORMATION: "CTGF amino acid sequence"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	Thr	Ala	Ala	Ser	Met	Gly	Pro	Val	Arg	Val	Ala	Phe	Val	Val	Leu	
1				5					10					15		
Leu	Ala	Leu	Cys	Ser	Arg	Pro	Ala	Val	Gly	Gln	Asn	Cys	Ser	Gly	Pro	
			20					25					30			
Cys	Arg	Cys	Pro	Asp	Glu	Pro	Ala	Pro	Arg	Cys	Pro	Ala	Gly	Val	Ser	
			35				40					45				
Leu	Val	Leu	Asp	Gly	Cys	Gly	Cys	Cys	Arg	Val	Cys	Ala	Lys	Gln	Leu	
	50					55					60					
Gly	Glu	Leu	Cys	Thr	Glu	Arg	Asp	Pro	Cys	Asp	Pro	His	Lys	Gly	Leu	
65					70					75					80	
Phe	Cys	Asp	Phe	Gly	Ser	Pro	Ala	Asn	Arg	Lys	Ile	Gly	Val	Cys	Thr	
				85					90					95		
Ala	Lys	Asp	Gly	Ala	Pro	Cys	Ile	Phe	Gly	Gly	Thr	Val	Tyr	Arg	Ser	
			100					105					110			
Gly	Glu	Ser	Phe	Gln	Ser	Ser	Cys	Lys	Tyr	Gln	Cys	Thr	Cys	Leu	Asp	
		115					120					125				
Gly	Ala	Val	Gly	Cys	Met	Pro	Leu	Cys	Ser	Met	Asp	Val	Arg	Leu	Pro	
	130					135					140					
Ser	Pro	Asp	Cys	Pro	Phe	Pro	Arg	Arg	Val	Lys	Leu	Pro	Gly	Lys	Cys	
145					150					155					160	
Cys	Glu	Glu	Trp	Val	Cys	Asp	Glu	Pro	Lys	Asp	Gln	Thr	Val	Val	Gly	
				165					170					175		
Pro	Ala	Leu	Ala	Ala	Tyr	Arg	Leu	Glu	Asp	Thr	Phe	Gly	Pro	Asp	Pro	
			180					185					190			
Thr	Met	Ile	Arg	Ala	Asn	Cys	Leu	Val	Gln	Thr	Thr	Glu	Trp	Ser	Ala	
		195					200					205				
Cys	Ser	Lys	Thr	Cys	Gly	Met	Gly	Ile	Ser	Thr	Arg	Val	Thr	Asn	Asp	
	210					215					220					
Asn	Ala	Ser	Cys	Arg	Leu	Glu	Lys	Gln	Ser	Arg	Leu	Cys	Met	Val	Arg	
225					230					235					240	
Pro	Cys	Glu	Ala	Asp	Leu	Glu	Glu	Asn	Ile	Lys	Lys	Gly	Lys	Lys	Cys	
				245					250					255		
Ile	Arg	Thr	Pro	Lys	Ile	Ser	Lys	Pro	Ile	Lys	Phe	Glu	Leu	Ser	Gly	
			260					265					270			
Cys	Thr	Ser	Met	Lys	Thr	Tyr	Arg	Ala	Lys	Phe	Cys	Gly	Val	Cys	Thr	
		275					280					285				

Asp	Gly	Arg	Cys	Cys	Thr	Pro	His	Arg	Thr	Thr	Thr	Leu	Pro	Val	Glu
290							295					300			
Phe	Lys	Cys	Pro	Asp	Gly	Glu	Val	Met	Lys	Lys	Asn	Met	Met	Phe	Ile
305					310					315					320
Lys	Thr	Cys	Ala	Cys	His	Tyr	Asn	Cys	Pro	Gly	Asp	Asn	Asp	Ile	Phe
				325					330					335	
Glu	Ser	Leu	Tyr	Tyr	Arg	Lys	Met	Tyr	Gly	Asp	Met	Ala			
			340					345							

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGGGATCTGT GACGAGCCCA AGGAC

25

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGGAATTCGA CCAGGCAGTT GGCTCG

26

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGGGATCCTG TGATGAAGAC AGCATT

26

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GGGAATTCAA CGATGCATTT CTGGCC

26

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Asp	Gly	Cys	Gly	Cys	Cys	Lys	Val	Cys	Ala	Lys	Gln	Leu	Asn	Glu	Asp
1				5					10					15	

Cys	Ser	Lys	Thr	Gln
				20

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Pro Asn Cys Lys His Gln Cys Thr Cys Ile Asp Gly Ala Val Gly Cys
1 5 10 15

Ile Pro Leu Cys Pro
 20

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Cys Ile Val Gln Thr Thr Ser Trp Ser Gln Cys Ser Lys Ser Cys Gly
1 5 10 15

Thr Gly Ile Ser Thr Arg Val Thr
 20

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Ile Ser Thr Arg Val Thr Asn Asp Asn Pro Glu Cys Arg Leu Val Lys
1 5 10 15

Glu Thr Arg Ile Cys Glu Val Arg Pro Cys
 20 25

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant

(D) TOPOLOGY: not relevant
(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Lys	Tyr	Cys	Gly	Ser	Cys	Val	Asp	Gly	Arg	Cys	Cys	Thr	Pro	Leu	Gln
1				5				10						15	
Thr	Arg	Thr	Val	Lys											
					20										

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

gggaattctg tcgggatctg tctgtcaaga gtgctg

36

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ccggatccga cagattgata gattgaca

28

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 375 base pairs
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met 1	Gly	Ser	Ala	Gly 5	Ala	Arg	Pro	Ala	Leu 10	Ala	Ala	Ala	Leu	Leu 15	Cys
Leu	Ala	Arg	Leu	Ala	Leu	Gly	Ser	Pro	Cys	Pro	Ala	Val	Cys	Gln	Cys
			20				25						30		
Pro	Ala	Ala	Ala	Pro	Gln	Cys	Ala	Pro	Gly	Val	Gly	Leu	Val	Pro	Asp
		35					40					45			
Gly	Cys	Gly	Cys	Cys	Lys	Val	Cys	Ala	Lys	Gln	Leu	Asn	Glu	Asp	Cys
		50				55					60				
Ser	Arg	Thr	Gln	Pro	Cys	Asp	His	Thr	Lys	Gly	Leu	Glu	Cys	Asn	Phe
65				70						75				80	
Gly	Ala	Ser	Pro	Ala	Ala	Thr	Asn	Gly	Ile	Cys	Arg	Ala	Gln	Ser	Glu
			85						90					95	
Gly	Arg	Pro	Cys	Glu	Tyr	Asn	Ser	Lys	Ile	Tyr	Gln	Asn	Gly	Glu	Ser
			100					105					110		
Phe	Gln	Pro	Asn	Cys	Lys	His	Gln	Cys	Thr	Cys	Ile	Asp	Gly	Ala	Val
		115					120					125			
Gly	Cys	Ile	Pro	Leu	Cys	Pro	Gln	Glu	Leu	Ser	Leu	Pro	Asn	Leu	Gly
	130					135					140				
Cys	Pro	Ser	Pro	Arg	Leu	Val	Lys	Val	Pro	Gly	Gln	Cys	Cys	Glu	Glu
145				150						155				160	
Trp	Val	Cys	Asp	Glu	Ser	Lys	Asp	Ala	Leu	Glu	Glu	Leu	Glu	Gly	Phe
			165						170					175	
Phe	Ser	Lys	Glu	Phe	Gly	Leu	Asp	Ala	Ser	Glu	Gly	Glu	Leu	Thr	Arg
			180					185					190		
Asn	Asn	Glu	Leu	Ile	Ala	Ile	Val	Lys	Gly	Gly	Leu	Lys	Met	Leu	Pro
		195					200					205			
Val	Phe	Gly	Ser	Glu	Pro	Gln	Ser	Arg	Ala	Phe	Glu	Asn	Pro	Lys	Cys
	210					215					220				
Ile	Val	Gln	Thr	Thr	Ser	Trp	Ser	Gln	Cys	Ser	Lys	Thr	Cys	Gly	Thr
225				230						235				240	
Gly	Ile	Ser	Thr	Arg	Val	Thr	Asn	Asp	Asn	Pro	Asp	Cys	Lys	Leu	Ile
			245						250					255	
Lys	Glu	Thr	Arg	Ile	Cys	Glu	Val	Arg	Pro	Cys	Gly	Gln	Pro	Ser	Tyr
			260					265					270		
Ala	Ser	Leu	Lys	Lys	Gly	Lys	Lys	Cys	Thr	Lys	Thr	Lys	Lys	Ser	Pro
		275					280					285			
Ser	Pro	Val	Arg	Phe	Thr	Tyr	Ala	Gly	Cys	Ser	Ser	Val	Lys	Lys	Tyr
	290					295					300				
Arg	Pro	Lys	Tyr	Cys	Gly	Ser	Cys	Val	Asp	Gly	Arg	Cys	Cys	Thr	Pro
305				310						315				320	
Gln	Gln	Thr	Arg	Thr	Val	Lys	Ile	Arg	Phe	Arg	Cys	Asp	Asp	Gly	Glu
			325						330					335	
Thr	Phe	Thr	Lys	Ser	Val	Met	Met	Ile	Gln	Ser	Cys	Arg	Cys	Asn	Tyr
			340					345					350		
Asn	Cys	Pro	His	Ala	Asn	Glu	Ala	Tyr	Pro	Phe	Tyr	Arg	Leu	Val	Asn
		355													

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met	Glu	Thr	Gly	Gly	Gly	Gln	Gly	Leu	Pro	Val	Leu	Leu	Leu	Leu	Leu
1				5				10						15	
Leu	Leu	Leu	Arg	Pro	Cys	Glu	Val	Ser	Gly	Arg	Glu	Ala	Ala	Cys	Pro
			20					25					30		
Arg	Pro	Cys	Gly	Gly	Arg	Cys	Pro	Ala	Glu	Pro	Pro	Arg	Cys	Ala	Pro
			35				40					45			
Gly	Val	Pro	Ala	Val	Leu	Asp	Gly	Cys	Gly	Cys	Cys	Leu	Val	Cys	Ala
	50					55					60				
Arg	Gln	Arg	Gly	Glu	Ser	Cys	Ser	Pro	Leu	Leu	Pro	Cys	Asp	Glu	Ser
65					70					75				80	
Gly	Gly	Leu	Tyr	Cys	Asp	Arg	Gly	Pro	Glu	Asp	Gly	Gly	Gly	Ala	Gly
				85					90					95	
Ile	Cys	Met	Val	Leu	Glu	Gly	Asp	Asn	Cys	Val	Phe	Asp	Gly	Met	Ile
			100					105					110		
Tyr	Arg	Asn	Gly	Glu	Thr	Phe	Gln	Pro	Ser	Cys	Lys	Tyr	Gln	Cys	Thr
			115				120					125			
Cys	Arg	Asp	Gly	Gln	Ile	Gly	Cys	Leu	Pro	Arg	Cys	Asn	Leu	Gly	Leu
			130			135					140				
Leu	Leu	Pro	Gly	Pro	Asp	Cys	Pro	Phe	Pro	Arg	Lys	Ile	Glu	Val	Pro
145					150					155				160	
Gly	Glu	Cys	Cys	Glu	Lys	Trp	Val	Cys	Asp	Pro	Arg	Asp	Glu	Val	Leu
				165					170				175		
Leu	Gly	Gly	Phe	Ala	Met	Ala	Ala	Tyr	Arg	Gln	Glu	Ala	Thr	Leu	Gly
			180					185				190			
Ile	Asp	Val	Ser	Asp	Ser	Ser	Ala	Asn	Cys	Ile	Glu	Gln	Thr	Thr	Glu
			195				200					205			
Trp	Ser	Ala	Cys	Ser	Lys	Ser	Cys	Gly	Met	Gly	Phe	Ser	Thr	Arg	Val
			210			215					220				
Thr	Asn	Arg	Asn	Gln	Gln	Cys	Glu	Met	Val	Lys	Gln	Thr	Arg	Leu	Cys
225				230						235				240	
Met	Met	Arg	Pro	Cys	Glu	Asn	Glu	Glu	Pro	Ser	Asp	Lys	Lys	Gly	Lys
				245					250					255	
Lys	Cys	Ile	Gln	Thr	Lys	Lys	Ser	Met	Lys	Ala	Val	Arg	Phe	Glu	Tyr
			260					265					270		
Lys	Asn	Cys	Thr	Ser	Val	Gln	Thr	Tyr	Lys	Pro	Arg	Tyr	Cys	Gly	Leu
			275				280					285			
Cys	Asn	Asp	Gly	Arg	Cys	Cys	Thr	Pro	His	Asn	Thr	Lys	Thr	Ile	Gln
			290			295					300				
Val	Glu	Phe	Arg	Cys	Pro	Gln	Gly	Lys	Phe	Leu	Lys	Lys	Pro	Met	Met
305					310					315				320	
Leu	Ile	Asn	Thr	Cys	Val	Cys	His	Gly	Asn	Cys	Pro	Gln	Ser	Asn	Asn
				325					330					335	

Ala Phe Phe Gln Pro Leu Asp Pro Met Ser Ser Glu Ala Lys Ile
340 345 350